

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:34:27 ; Search time 207.681 Seconds
(without alignments)
74.274 Million cell updates/sec

Title: US-09-830-954A-3

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGGVVIAT 43

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	222	100.0	43	2	AAR54759	Aar54759 Beta amyl
2	222	100.0	43	2	AAR60367	Aar60367 Beta-amyl
3	222	100.0	43	2	AAR61328	Aar61328 Amyloid b
4	222	100.0	43	2	AAR64165	Aar64165 Beta amyl
5	222	100.0	43	2	ADD11650	Add11650 Human bet
6	222	100.0	43	2	AAR95673	Aar95673 A-beta pr
7	222	100.0	43	2	AAW93371	Aaw93371 Human bet
8	222	100.0	43	2	AAY17758	Aay17758 Beta-amyl
9	222	100.0	43	2	AAW51316	Aaw51316 Natural b

10	222	100.0	43	2	AAY42955	Aay42955 Beta-amyl
11	222	100.0	43	2	AAB21216	Aab21216 Beta-amyl
12	222	100.0	43	2	AAW71378	Aaw71378 Beta-amyl
13	222	100.0	43	2	AAW40129	Aaw40129 Human amy
14	222	100.0	43	2	AAW89362	Aaw89362 Beta-amyl
15	222	100.0	43	3	AAY88390	Aay88390 Beta-amyl
16	222	100.0	43	3	AAY56102	Aay56102 Natural b
17	222	100.0	43	3	AAB27020	Aab27020 Beta-amyl
18	222	100.0	43	3	AAB15372	Aab15372 Human bet
19	222	100.0	43	4	ABB07901	Abb07901 Beta-amyl
20	222	100.0	43	4	AAB84428	Aab84428 Partial s
21	222	100.0	43	4	AAB91811	Aab91811 Amyloid b
22	222	100.0	43	4	AAB91778	Aab91778 Amyloid b
23	222	100.0	43	4	AAG78791	Aag78791 Human bet
24	222	100.0	43	4	AAB48344	Aab48344 Beta-amyl
25	222	100.0	43	4	AAB81193	Aab81193 Beta-amyl
26	222	100.0	43	4	AAB98986	Aab98986 Beta-amyl
27	222	100.0	43	4	AAB47108	Aab47108 Biotinyl a
28	222	100.0	43	4	AAE12508	Aae12508 Beta-amyl
29	222	100.0	43	5	ABB98516	Abb98516 Human bet
30	222	100.0	43	5	ABG71001	Abg71001 Natural l
31	222	100.0	43	5	AAO18457	Aao18457 Human bet
32	222	100.0	43	5	ABB05149	Abb05149 Beta amyl
33	222	100.0	43	5	AAU98701	Aau98701 Human amy
34	222	100.0	43	5	AAM50862	Aam50862 Beta-amyl
35	222	100.0	43	5	ABB78007	Abb78007 Amino aci
36	222	100.0	43	5	AAE26265	Aae26265 Human bet
37	222	100.0	43	6	AAO16064	Aao16064 Neurologi
38	222	100.0	43	6	ABG73456	Abg73456 Natural b
39	222	100.0	43	6	ABU08505	Abu08505 Human amy
40	222	100.0	43	6	ABP96145	Abp96145 Human Abe
41	222	100.0	43	6	ABR39273	Abr39273 Human Amy
42	222	100.0	43	6	ABP97881	Abp97881 Amino aci
43	222	100.0	43	6	ABU62720	Abu62720 Beta-amyl
44	222	100.0	43	7	ADC66003	Adc66003 Human A(b
45	222	100.0	43	7	ADI53072	Adi53072 Amyloid-b

ALIGNMENTS

RESULT 1

AAR54759

ID AAR54759 standard; peptide; 43 AA.

XX

AC AAR54759;

XX

DT 25-MAR-2003 (revised)

DT 30-NOV-1994 (first entry)

XX

DE Beta amyloid peptide.

XX

KW Beta amyloid peptide; amyloid plaques; Alzheimer's disease; lesion;

KW brain; senility; dementia; detection; diagnosis.

XX

OS Homo sapiens.

XX

PN WO9410569-A1.
XX
PD 11-MAY-1994.
XX
PF 01-SEP-1993; 93WO-US008264.
XX
PR 26-OCT-1992; 92US-00965972.
XX
PA (SCHE/) SCHENK D B.
PA (SCHL/) SCHLOSSMACHER M G.
PA (SELK/) SELKOE D J.
PA (SEUB/) SEUBERT P A.
PA (VIGO/) VIGO-PELFREY C.
XX
PI Schenk DB, Schlossmacher MG, Selkoe DJ, Seubert PA;
PI Vigo-Pelfrey C;
XX
DR WPI; 1994-167654/20.
XX
PT Detecting soluble beta-amyloid peptide concns. e.g. for diagnosing and
PT assessing progression of Alzheimer's disease - by exposing cultured cells
PT to test cpd. to determine effect of cpd. on produced soluble beta-amyloid
PT peptide.
XX
PS Disclosure; Page 10; 55pp; English.
XX
CC Beta amyloid peptide is the principal chemical constituent of amyloid
CC plaques, lesions found on the brains of Alzheimer's disease patients. The
CC ability to detect beta amyloid peptide in fluid samples provides a means
CC of diagnosing Alzheimer's disease. (Updated on 25-MAR-2003 to correct PN
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 2
AAR60367
ID AAR60367 standard; peptide; 43 AA.
XX
AC AAR60367;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX
DE Beta-amyloid (1-43).
XX
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.

XX
OS Homo sapiens.
XX
PN WO9417197-A1.
XX
PD 04-AUG-1994.
XX
PF 24-JAN-1994; 94WO-JP000089.
XX
PR 25-JAN-1993; 93JP-00010132.
PR 05-FEB-1993; 93JP-00019035.
PR 16-NOV-1993; 93JP-00286985.
PR 28-DEC-1993; 93JP-00334773.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Suzuki N, Odaka A, Kitada C;
XX
DR WPI; 1994-264110/32.
XX
PT Antibodies recognising specific parts of beta-amyloid - can be used for
PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
PT disease.
XX
PS Disclosure; Page 83; 116pp; Japanese.
XX
CC Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
CC the C-terminal portion. The antibodies are useful for assaying beta-
CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 3
AAR61328
ID AAR61328 standard; protein; 43 AA.
XX
AC AAR61328;
XX
DT 25-MAR-2003 (revised)
DT 21-APR-1995 (first entry)
XX
DE Amyloid beta-protein, ABP.
XX
KW Amyloid beta-protein; ABP; Tau-protein kinase I enzyme; TPK-I;

KW Alzheimer's disease.
XX
OS Synthetic.
XX
PN EP616032-A2.
XX
PD 21-SEP-1994.
XX
PF 01-MAR-1994; 94EP-00103057.
XX
PR 02-MAR-1993; 93JP-00041160.
PR 22-MAR-1993; 93JP-00085143.
PR 02-AUG-1993; 93JP-00191246.
XX
PA (MITU) MITSUBISHI KASEI CORP.
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A;
PI Sato S;
XX
DR WPI; 1994-287181/36.
XX
PT Newly isolated tau-protein kinase I enzyme - with specificity for tau-
PT protein providing means for prevention and treatment of Alzheimer's
PT disease.
XX
PS Example 1; Page 22; 30pp; English.
XX
CC Amyloid beta-protein (ABP) is the main component of senile plaques in
CC Alzheimer's disease. ABP was used to demonstrate the protective
CC properties of anti-sense TPK-I oligonucleotides (AAQ67461 and AAQ67462)
CC on hippocampus cells dosed with ABP. (Updated on 25-MAR-2003 to correct
CC PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 4
AAR64165
ID AAR64165 standard; peptide; 43 AA.
XX
AC AAR64165;
XX
DT 25-MAR-2003 (revised)
DT 02-AUG-1995 (first entry)
XX
DE Beta amyloid protein.
XX
KW beta amyloid protein; mutant; variant; detection; amyloid deposition;

KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
KW Down's syndrome.
XX
OS Synthetic.
XX
PN WO9428412-A1.
XX
PD 08-DEC-1994.
XX
PF 27-MAY-1994; 94WO-US005809.
XX
PR 28-MAY-1993; 93US-00069010.
XX
PA (MIRI-) MIRIAM HOSPITAL.
XX
PI Marotta CA, Majocha RE;
XX
DR WPI; 1995-023013/03.
XX
PT Amyloid binding composition comprising labelled amyloid protein and
PT carrier - useful for in vivo imaging of amyloid deposits, for diagnosing
PT Alzheimer's disease and Down's Syndrome.
XX
PS Claim 5; Page 42; 58pp; English.
XX
CC AAR64165 shows the amino acid sequence of the beta amyloid protein. The
CC protein binds amyloid and is useful for in vivo imaging of amyloid
CC deposits and hence diagnosis of an amyloidosis-associated disease, such
CC as Alzheimer's disease or Down's syndrome. AAR64165-69 show specific
CC variants generated from this generic sequence with addition amino acids.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 5
ADD11650
ID ADD11650 standard; protein; 43 AA.
XX
AC ADD11650;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human beta-amyloid 1-43 (beta1-43).
XX
KW neurotoxic effect; beta-amyloid peptide; neurotoxicity inhibitor;
KW amyloidogenic amylin; beta_2-microglobulin; amylin; Alzheimer's disease;
KW Down's syndrome; beta-amyloid neurotoxicity assay; human;
KW beta-amyloid 1-43; beta1-43.

XX
OS Homo sapiens.
XX
PN EP646792-A1.
XX
PD 05-APR-1995.
XX
PF 17-AUG-1994; 94EP-00306053.
XX
PR 19-AUG-1993; 93US-00109782.
XX
PA (ELIL) LILLY & CO ELI.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI May PC, Rydel RE;
XX
DR WPI; 1995-132760/18.
XX
PT Assay for effectiveness of agents used in the treatment of Alzheimer's
PT disease - by incubating potential inhibitor of neurotoxicity with amylin
PT or beta-2-microglobulin and measuring neurotoxic props. of mixt.
XX
PS Disclosure; SEQ ID NO 1; 14pp; English.
XX
CC The invention describes a method for assaying the effectiveness of agents
CC useful for ameliorating the neurotoxic effects of a condition associated
CC with the accumulation of a beta-amyloid peptide. The method comprises:
CC (a) incubating potential inhibitors of neurotoxicity with an
CC amyloidogenic amylin or beta_2-microglobulin; (b) measuring the
CC neurotoxic properties of each amylin or beta_2-microglobulin/potential
CC inhibitor mixture; and (c) detecting reduction in the neurotoxicity
CC relative to a control. The preferred amyloidogenic amylin is human
CC amylin. The method is especially for assessing the ability of an agent to
CC ameliorate the neurotoxic effects of Alzheimer's disease or Down's
CC syndrome. The method provides a more consistent beta-amyloid
CC neurotoxicity assay and is more sensitive and covers a broader range.
CC This is the amino acid sequence of human beta-amyloid 1-43 (beta1-43).
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 6
AAR95673
ID AAR95673 standard; peptide; 43 AA.
XX
AC AAR95673;
XX
DT 24-FEB-1997 (first entry)
XX

DE A-beta protein (43 amino acid version).
XX
KW A-beta protein; beta-amyloid precursor protein; APP; Alzheimer's disease;
KW diagnosis; monitor; amyloid plaque; senile.
XX
OS Homo sapiens.
XX
PN WO9615452-A1.
XX
PD 23-MAY-1996.
XX
PF 13-NOV-1995; 95WO-US014659.
XX
PR 14-NOV-1994; 94US-00339141.
PR 07-APR-1995; 95US-00419008.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Seubert PA, Vigo-Pelfrey C, Schenk DB, Barbour R;
XX
DR WPI; 1996-260003/26.
XX
PT Diagnosis and monitoring of Alzheimer's disease - by detecting abnormally
PT low concentration of A-beta peptide extending beyond amino acid 41 in
PT cerebrospinal fluid.
XX
PS Disclosure; Page 16; 57pp; English.
XX
CC The "amyloid-beta peptide" or A-beta is an approx. 4.2 kD protein which,
CC in the brains of Alzheimer's disease, Down's Syndrome, HCHWA-D and some
CC normal aged subjects, forms the subunit of amyloid filaments comprising
CC the senile (amyloid) plaques and the amyloid deposits in small cerebral
CC and meningeal blood vessels. A-beta is an approx. 39-43 amino acid
CC fragment of a large membrane-spanning glycoprotein, referred to as the
CC beta-amyloid precursor protein (APP), encoded by a gene on the long arm
CC of human chromosome 21. Detecting the amt. of A-beta is useful in
CC diagnosis and monitoring of Alzheimer's disease, when taken together with
CC other clinical symptoms. The present sequence is a 43 amino acid version
CC of A-beta
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 7
AAW93371
ID AAW93371 standard; protein; 43 AA.
XX
AC AAW93371;
XX

DT 28-MAY-1999 (first entry)

XX

DE Human beta-amyloid polypeptide.

XX

KW Cathepsin Y; human; beta-amyloid peptide; BAP; secretion; inhibitor; protease; carboxypeptidase; aliphatic C-terminal amino acid; diagnostic; glycoprotein; cerebral deposition; pathogenesis; Alzheimer's disease; detection; amyloid plaque; angiopathy; brain; Trisomy 21; amyloidosis; Down's syndrome; hereditary cerebral haemorrhage.

XX

OS Homo sapiens.

XX

PN WO9639194-A1.

XX

PD 12-DEC-1996.

XX

PF 26-APR-1996; 96WO-US006211.

XX

PR 06-JUN-1995; 95US-00467607.

PR 06-JUN-1995; 95US-00469362.

XX

PA (ATHE-) ATHENA NEUROSCIENCES INC.

XX

PI Tung JS, Sinha S, Mcconlogue L, Tatsuno G, Anderson J, Semko CMF;

PI Chrysler S;

XX

DR WPI; 1997-042872/04.

XX

PT Acylamino and acyl:peptido:amino alcohol and aldehyde derivs. - inhibit
PT beta-amyloid peptide prodn. in cells, use in Alzheimer's disease, also
PT prepn. of cathepsin Y and nucleic acid encoding for it.

XX

PS Disclosure; Page 11; 90pp; English.

XX

CC This invention describes the inhibition of beta-amyloid peptide
CC production in cells is effected by administration of an acylamino or
CC acylpeptidoamino alcohol or aldehyde derivative of formula R1(X)m--Y--NR--
CC -CHR2-[CONR10-CHR3]n-R4 where R and R10 = H or 1-6C alkyl; or R and R2
CC together, and/or R10 and R3 together complete a 4-10C ring structure; R1
CC = (a) 1-4C alkyl substd. by 1-5 substs. chosen from 6-10C aryl (opt.
CC substd. by 1-3 of 1-6C alkyl, 1-6C alkoxy, 6-10C aryl, 6-10C aryloxy, OH,
CC cyano, halo and amino), 3-8C cycloalkyl or Het, in which the substd.
CC alkyl gp. is opt. further substd. by 1 or 2 of OH; (b) 2-4C alkenyl
CC substd. by 1-4 substs. as for 1-4C alkyl above; (c) 6-10C aryl (opt.
CC substd. by 1-3 substs. as for alkyl above), (d) fluorenyl or (e) Het;
CC Het = 3-14C heterocyclyl contg. 1-3 N, O or S heteroatoms; R2 and R3 = D-
CC or L- amino acid side chains of at least 2C atoms, excluding prolyl side
CC chain; R4 = COCH=N2, CH2OH, C=NOH or COR5; R5 = H, 1-6C alkyl (opt.
CC contg. 1 or 2 halogen atoms), 1-6C alkoxy, NR6R7 or N(Me)OMe; R6 and R7 =
CC H or 1-6C alkyl; X = O, NR9 or S; R9 = H, 1-6C alkyl or 6-10C aryl; Y =
CC CO or CS; m = 0 or 1; and n = 0-2; provided that (i) when R1 = 1-
CC naphthyl, R2 = CHMe2 (L-isomer), R3 = benzyl (L-isomer), Y = CO, m = 0
CC and n = 1, then R4 (sic) is not N(Me)OMe; (ii) when R1 = CHPh2, R2 = p-
CC benzyloxybenzyl (L-isomer), Y = CO, and m = n = 0, then R4 (sic) is not
CC N(Me)OMe; and (iii) when R1 = PhCH=CPh, Y = CO, R2 = benzyl (L-isomer)
CC and m = n = 0, then R4 (sic) is not N(Me)OMe. Cathepsin Y is a 31 kD
CC carboxypeptidase with particular activity for aliphatic C-terminal amino

CC acids. It is involved in the generation of beta-amyloid protein (BAP)
CC from its precursor glycoprotein. Cerebral deposition of BAP plays a key
CC role in pathogenesis of Alzheimer's disease (AD), and its detection can
CC precede openly apparent symptoms of AD by years or more. Amyloid plaques
CC and angiopathy are also present in the brain in those having Trisomy 21
CC (Down's syndrome) and hereditary cerebral haemorrhage with amyloidosis of
CC Dutch type (HCHWA-D). The inhibitors are of use in inhibiting such plaque
CC deposition and in treating AD. The cathepsin Y can be used, by virtue of
CC its carboxypeptidase activity, in screening for BAP prodn. inhibitors,
CC and, more widely, as a general C-terminal protease in a variety of
CC chemical and biological systems. Conversely, assay of cathepsin Y in body
CC fluid can be used diagnostically to evaluate the future risk of
CC developing AD. The nucleic acid can be used to probe specifically for
CC presence of cathepsin Y RNA or DNA in tissues or cloned libraries. It can
CC also be used for expression of recombinant cathepsin Y, by transfection
CC of a host cell

XX

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVIA 43

|||||||||||||||||||||||||||||||||||||||||||||

Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVIA 43

RESULT 8

AAY17758

ID AAY17758 standard; peptide; 43 AA.

XX

AC AAY17758;

XX

DT 10-AUG-1999 (first entry)

XX

DE Beta-amyloid peptide.

XX

KW Beta-amyloid peptide; beta-amyloid precursor protein; APP;
KW membrane spanning glycoprotein; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO9822493-A2.

XX

PD 28-MAY-1998.

XX

PF 20-NOV-1997; 97WO-US018704.

XX

PR 22-NOV-1996; 96US-00755334.

XX

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PA (ELIL) LILLY & CO ELI.

XX

PI Audia JE, Folmer BK, John V, Latimer LH, Nissen JS, Porter WJ;

PI Thorsett ED, Wu J;

XX

DR WPI; 1998-322359/28.

XX

PT New and known aryl or hetero-aryl amino acid derivatives - useful for
PT inhibiting beta-amyloid peptide release and/or its synthesis and treating
PT Alzheimer's disease.

XX

PS Disclosure; Page 19; 131pp; English.

XX

CC The present invention describes a composition comprising an inert carrier
CC and an N-(aryl or heteroaryl) amino acid derivative e.g. N-[N-(3,4-
CC dichlorophenyl)alanyl] valine methyl ester. The composition can be used
CC for inhibiting beta-amyloid peptide release and/or its synthesis in a
CC cell, for preventing the onset of Alzheimer's disease and for treating
CC Alzheimer's disease in order to inhibit further deterioration. The dosage
CC is 0.1-500 mg/kg/day orally, rectally, transdermally, subcutaneously or
CC intravenously. The present sequence represents the beta-amyloid peptide

XX

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

||||||||||||||||||||||||||||||||||||||||||||||

Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 9

AAW51316

ID AAW51316 standard; peptide; 43 AA.

XX

AC AAW51316;

XX

DT 14-AUG-1998 (first entry)

XX

DE Natural beta-amyloid peptide fragment.

XX

KW Natural beta-amyloid peptide; aggregation; D-amino acid;
KW Alzheimer's disease; beta-amyloidosis.

XX

OS Homo sapiens.

XX

PN WO9808868-A1.

XX

PD 05-MAR-1998.

XX

PF 27-AUG-1997; 97WO-US015166.

XX

PR 27-AUG-1996; 96US-00703675.

PR 21-JUL-1997; 97US-00897342.

XX

PA (PRAE-) PRAECIS PHARM INC.

XX

PI Findeis MA, Gefter ML, Musso G, Signer ER, Wakefield J;
PI Molineaux S, Chin J, Lee J, Kelley M, Komar-Panicucci S;
PI Arico-Muendel CC, Phillips K, Hayward NJ;

XX
DR WPI; 1998-216936/19.
XX
PT Peptide compounds which are preferably based on beta-amyloid peptide(s) -
PT are useful in treatment of disorders related to beta-amyloidosis,
PT especially Alzheimer's disease.
XX
PS Disclosure; Page 8; 92pp; English.
XX
CC The invention relates to peptides that modulate natural beta-amyloid
CC peptide aggregation. The modulators of the invention comprise a peptide
CC preferably based on a beta-amyloid peptide, that is comprised entirely of
CC D-amino acids. Preferably the peptide comprises 3-5 D-amino acid residues
CC and includes at least two D-amino acid residues independently selected
CC from the group consisting of D-leucine, D-phenylalanine and D-valine.
CC Preferred amino-terminal modifying groups include cyclic, heterocyclic,
CC polycyclic and branched alkyl groups. Preferred carboxy-terminal
CC modifying groups include an amide group, an alkyl amide group, an aryl
CC amide group or a hydroxy group. The peptides may be used to treat
CC disorders associated with beta-amyloidosis, especially Alzheimer's
CC disease. They may also be used in methods for detecting the presence of
CC beta-amyloid peptides in biological samples. The present sequence
CC represents the 43 amino acid long form of natural beta-amyloid peptide
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 10
AAY42955
ID AAY42955 standard; protein; 43 AA.
XX
AC AAY42955;
XX
DT 02-JAN-2000 (first entry)
XX
DE Beta-amyloid precursor protein.
XX
KW Beta-amyloid precursor protein protein; APP; release inhibition;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5965614-A.
XX
PD 12-OCT-1999.
XX
PF 21-NOV-1997; 97US-00975977.
XX
PR 22-NOV-1996; 96US-00755444.

PR 22-NOV-1996; 96US-0104593P.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Folmer BK, Audia JE, Latimer LH, Nissen JS, Reel JK, Thorsett ED;
PI Whitesitt CA, John V;
XX
DR WPI; 1998-348125/30.
XX
PT N-Aryl- and N-hetero-aryl-amino acid ester(s) and amidoxime ester(s) -
PT are inhibitors of beta-amyloid peptide synthesis and/or release, used in
PT treating Alzheimer's disease.
XX
PS Disclosure; Col 49; 29pp; English.
XX
CC New chemical compounds are disclosed which inhibit the cellular release
CC and/or synthesis of beta-amyloid peptide (the present sequence). The
CC compounds are N-(aryl or heteroaryl) amino acid ester derivatives, of
CC which N-(3,4-dichlorophenyl)alanine ethyl ester is a specific example.
CC These compounds can be used for the treatment and prevention of
CC Alzheimer's disease
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 11
AAB21216
ID AAB21216 standard; peptide; 43 AA.
XX
AC AAB21216;
XX
DT 11-JAN-2001 (first entry)
XX
DE Beta-amyloid peptide.
XX
KW Beta-amyloid peptide; membrane-spanning glycoprotein; analgesic;
KW nicotinic agonist; beta-amyloid precursor protein; APP;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US6117901-A.
XX
PD 12-SEP-2000.
XX
PF 21-NOV-1997; 97US-00976179.
XX
PR 22-NOV-1996; 96US-00754895.
PR 22-NOV-1996; 96US-0098551P.

XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PA (ELIL) LILLY & CO ELI.
XX
PI Thorsett ED, Nissen JS, Wu J, Latimer LH, John V, Fang LY;
PI Audia JE, Mabry TE;
XX
DR WPI; 1998-348123/30.
XX
PT New and use of substituted amino acid ester or thio-ester(s) - as
PT inhibitors or beta-amyloid peptide release and/or synthesis used in the
PT treatment and/or prevention of Alzheimer's disease.
XX
PS Disclosure; Col 11; 32pp; English.
XX
CC The present sequence is the beta-amyloid peptide, which is part of a
CC large membrane-spanning glycoprotein, referred to as the beta-amyloid
CC precursor protein (APP). Aryl substituted olefinic amine (metanicotine)
CC compounds which inhibit beta-amyloid peptide release and/or its synthesis
CC may be useful for treating Alzheimer's disease, both prophylactically and
CC therapeutically
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 12
AAW71378
ID AAW71378 standard; peptide; 43 AA.
XX
AC AAW71378;
XX
DT 02-DEC-1998 (first entry)
XX
DE Beta-amyloid precursor protein epitope.
XX
KW Beta amyloid precursor protein; eukaryotic cell line;
KW exogenous gene construction; identification; quantification; inhibitor;
KW beta-amyloid processing; treatment; Alzheimer's disease; brain trauma;
KW Downs syndrome.
XX
OS Homo sapiens.
XX
PN WO9837215-A1.
XX
PD 27-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US001899.
XX
PR 24-FEB-1997; 97US-00804971.

PR 02-APR-1997; 97US-00825737.
PR 31-JUL-1997; 97US-00904296.
XX
PA (HMRI) HOECHST MARION ROUSSEL INC.
PA (SCIO-) SCIOS INC.
XX
PI Cordell B, Scardina JM, Mischak RP, Huggins J, Pruss R;
PI Rautmann G;
XX
DR WPI; 1998-495368/42.
XX
PT New eukaryotic cell lines - contain a gene construct containing a beta-
PT amyloid precursor protein encoding sequence, used for identifying
PT inhibitors of beta-amyloid processing.
XX
PS Disclosure; Fig 5; 82pp; English.
XX
CC The present sequence represents an epitope derived from a beta amyloid
CC precursor protein, and recognised by antibodies BA#1, 108.1, 1702.1, and
CC 1101.1. The specification describes an eukaryotic cell line having
CC exogenous gene construction comprising a cytomegalovirus (CMV) promoter,
CC a strong ribosome binding site (RBS), a beta-amyloid precursor protein
CC (BAPP) nucleic acid sequence, a selectable marker, and a poly-adenylation
CC signal. The products can be used for identifying or quantifying beta-
CC amyloid protein and for identifying inhibitors of beta-amyloid
CC processing. They can be used to develop products for treating
CC amyloidoses, e.g. Alzheimer's disease, brain trauma or Downs syndrome
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 13
AAW40129
ID AAW40129 standard; peptide; 43 AA.
XX
AC AAW40129;
XX
DT 03-JUN-1998 (first entry)
XX
DE Human amyloid-beta peptide.
XX
KW Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiopathy; brain;
KW membrane-spanning glycoprotein; beta-amyloid precursor protein; APP;
KW chromosome 21; human; Alzheimers disease; AD; amyloid filament;
KW treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.
XX
OS Homo sapiens.
XX
PN WO9748983-A1.

XX
PD 24-DEC-1997.
XX
PF 18-JUN-1997; 97WO-US010601.
XX
PR 18-JUN-1996; 96US-00665649.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Citron M, Selkoe DJ, Seubert PA, Schenk D;
XX
DR WPI; 1998-063287/06.
XX
PT Identifying compounds that alter cellular production of amyloid-beta 42
PT fragment - in vitro or in transgenic animal models, potentially useful
PT for treatment of Alzheimer's and other amyloid deposition diseases.
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence represents a human amyloid-beta peptide (A-beta) which is a
CC fragment of the of a large membrane-spanning glycoprotein referred to as
CC the beta-amyloid precursor protein (APP) encoded by a gene on the long
CC arm of chromosome 21. This peptide is also known as the beta-AP peptide
CC and forms the subunit of the amyloid filaments comprising senile
CC (amyloid) plaques and the amyloid deposits in small cerebral and
CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be a
CC 39-43 amino acid fragment. This invention provides methods of screening
CC compounds for their ability to alter the production of the A-beta
CC peptide, which is composed of >41 amino acids, alone, or in combination
CC with the A-beta peptide composed of 40 amino acids or less. Such agents
CC that reduce the production of the A-beta peptide are potentially useful
CC for treatment of Alzheimers Disease or other diseases involving amyloid
CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with
CC amyloidosis of Dutch type and advanced aging of the brain
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 14
AAW89362
ID AAW89362 standard; peptide; 43 AA.
XX
AC AAW89362;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-1-43.
XX

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein; aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy; familial amyloid polyneuropathy; bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-00612785.
XX
PR 14-MAR-1995; 95US-00404831.
PR 07-JUN-1995; 95US-00475579.
PR 27-OCT-1995; 95US-00548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Hundal A, Gefter ML, Kasman L, Musso G, Molineaux S, Benjamin H;
PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
PI Garnick MB, Kubasek W, Signer ER;
XX
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit amyloid aggregation - and neurotoxicity, specifically for treatment and prevention of Alzheimer's disease.
XX
PS Example 1; Col 46; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and peptides, specifically bAP, and their neurotoxicity, so are useful for treating and preventing any disease involving amyloidosis, specifically Alzheimer's disease but also Down's syndrome, familial amyloid polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose these diseases, in vitro or in vivo, by detecting binding of bAP to labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation even when bAP is present in molar excess. The present sequence represents a bAP derivative
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 15
AY88390

ID AAY88390 standard; protein; 43 AA.
XX
AC AAY88390;
XX
DT 25-JUL-2000. (first entry)
XX
DE Beta-amyloid peptide amino acid sequence.
XX
KW Beta-amyloid peptide; Alzheimer's disease; inhibitor; treatment.
XX
OS Unidentified.
XX
PN WO200019210-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022684.
XX
PR 30-SEP-1998; 98US-0160082P.
XX
PA (ELAN-) ELAN PHARM INC.
PA (ELIL) LILLY & CO ELI.
XX
PI Audia JE, Hyslop PA, Nissen JS, Thompson RC, Tung JS, Tanner LI;
XX
DR WPI; 2000-328743/28.
XX
PT New reagents which bind factors involved in production of beta-amyloid
PT peptide, useful for developing drugs for use in treatment of Alzheimer's
PT disease.
XX
PS Disclosure; Page 14-15; 86pp; English.
XX
CC This amino acid sequence represents the beta-amyloid peptide, which is a
CC fragment of the larger amyloid precursor protein (APP). Brains of
CC patients with Alzheimer's disease have characteristic lesions termed
CC senile or amyloid plaques, the principle constituent of which is the beta
CC -amyloid peptide. The invention relates to biological reagents which
CC inhibit beta-amyloid release and/or its synthesis. The reagents can be
CC used to determine the cellular mechanism involved in the generation of
CC the beta-amyloid peptide. The compounds can also be used to identify
CC cells which express a cellular agent, such as peptides or proteins
CC involved with beta-amyloid peptide release and/or its synthesis. Such
CC methods can be used to provide drug design for agents which target
CC Alzheimer's disease
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

Search completed: November 19, 2004, 16:54:10
Job time : 210.681 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:39:17 ; Search time 50.3191 Seconds
(without alignments)
56.672 Million cell updates/sec

Title: US-09-830-954A-3

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGGVVIAT 43

Scoring table: BLOSUM62
Gapext 0.5, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	222	100.0	43	1	US-08-235-400-1	Sequence 1, Appli
2	222	100.0	43	1	US-08-437-067-1	Sequence 1, Appli
3	222	100.0	43	1	US-08-302-808-6	Sequence 6, Appli
4	222	100.0	43	1	US-08-079-511-1	Sequence 1, Appli
5	222	100.0	43	1	US-08-467-607-1	Sequence 1, Appli
6	222	100.0	43	2	US-08-404-831-1	Sequence 1, Appli
7	222	100.0	43	2	US-08-602-264A-3	Sequence 3, Appli
8	222	100.0	43	2	US-08-469-362-1	Sequence 1, Appli
9	222	100.0	43	2	US-08-612-785B-1	Sequence 1, Appli
10	222	100.0	43	2	US-08-475-579A-1	Sequence 1, Appli
11	222	100.0	43	2	US-08-850-392-1	Sequence 1, Appli

12	222	100.0	43	2	US-08-986-948-6	Sequence 6, Appli
13	222	100.0	43	2	US-08-975-977-1	Sequence 1, Appli
14	222	100.0	43	2	US-08-817-423-1	Sequence 1, Appli
15	222	100.0	43	2	US-08-920-162A-1	Sequence 1, Appli
16	222	100.0	43	3	US-08-461-018A-3	Sequence 3, Appli
17	222	100.0	43	3	US-08-976-191-1	Sequence 1, Appli
18	222	100.0	43	3	US-08-976-179-1	Sequence 1, Appli
19	222	100.0	43	3	US-09-216-958-3	Sequence 3, Appli
20	222	100.0	43	3	US-09-356-931-1	Sequence 1, Appli
21	222	100.0	43	3	US-08-733-202-1	Sequence 1, Appli
22	222	100.0	43	3	US-08-703-675C-1	Sequence 1, Appli
23	222	100.0	43	3	US-09-390-692-1	Sequence 1, Appli
24	222	100.0	43	3	US-08-617-267C-1	Sequence 1, Appli
25	222	100.0	43	3	US-09-303-655-1	Sequence 1, Appli
26	222	100.0	43	3	US-08-294-819-1	Sequence 1, Appli
27	222	100.0	43	4	US-09-408-283-1	Sequence 1, Appli
28	222	100.0	43	4	US-09-280-966-1	Sequence 1, Appli
29	222	100.0	43	4	US-09-032-019-1	Sequence 1, Appli
30	222	100.0	43	4	US-09-481-980A-1	Sequence 1, Appli
31	222	100.0	43	4	US-09-594-366-1	Sequence 1, Appli
32	222	100.0	43	4	US-08-665-649-1	Sequence 1, Appli
33	222	100.0	43	4	US-09-915-342-1	Sequence 1, Appli
34	222	100.0	43	4	US-08-996-422-1	Sequence 1, Appli
35	222	100.0	43	4	US-09-984-834-1	Sequence 1, Appli
36	222	100.0	43	4	US-09-027-258-2	Sequence 2, Appli
37	222	100.0	43	4	US-09-895-443A-1	Sequence 1, Appli
38	222	100.0	43	4	US-09-904-987-1	Sequence 1, Appli
39	222	100.0	43	4	US-10-314-221-1	Sequence 1, Appli
40	222	100.0	43	4	US-10-267-017-1	Sequence 1, Appli
41	222	100.0	47	2	US-08-609-090-10	Sequence 10, Appli
42	222	100.0	48	4	US-09-560-883-1	Sequence 1, Appli
43	222	100.0	52	2	US-08-609-090-11	Sequence 11, Appli
44	222	100.0	53	3	US-09-173-887-5	Sequence 5, Appli
45	222	100.0	53	4	US-09-797-543-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
 US-08-235-400-1
 ; Sequence 1, Application US/08235400
 ; Patent No. 5552426
 ; GENERAL INFORMATION:
 ; APPLICANT: Lunn, William H.
 ; APPLICANT: Monn, James A.
 ; APPLICANT: Zimmerman, Dennis M.
 ; TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
 ; TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eli Lilly and Company
 ; STREET: Lilly Corporate Center/1104
 ; CITY: Indianapolis
 ; STATE: Indiana
 ; COUNTRY: United States of America
 ; ZIP: 46285

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,400
;
; FILING DATE:
; CLASSIFICATION: 514
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9507
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-235-400-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 2
US-08-437-067-1
;
; Sequence 1, Application US/08437067
;
; Patent No. 5593846
;
; GENERAL INFORMATION:
;
; APPLICANT: Schenk, Dale B.
;
; APPLICANT: Selkoe, Dennis J.
;
; APPLICANT: Schlossmacher, Michael G.
;
; APPLICANT: Seubert, Peter A.
;
; APPLICANT: Vigo-Pelfrey, Carmen
;
; TITLE OF INVENTION: Methods and Compositions for
;
; TITLE OF INVENTION: Detection
;
; TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
;
; NUMBER OF SEQUENCES: 4
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Townsend and Townsend
;
; STREET: One Market Plaza, Steuart Tower, Suite 2000
;
; CITY: San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94105
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,067
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,972
; FILING DATE: 26-OCT-1992
; APPLICATION NUMBER: US 07/911,647
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-6-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-437-067-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 3
US-08-302-808-6
; Sequence 6, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-6

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 4
US-08-079-511-1
; Sequence 1, Application US/08079511
; Patent No. 5766846
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Selkoe, Dennis J.
; APPLICANT: Schlossmacher, Michael G.
; APPLICANT: Seubert, Peter A.

; APPLICANT: Vigo-Pelfrey, Carmen
; TITLE OF INVENTION: Methods and Compositions for Detection
; TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/079,511
; FILING DATE: 19930617
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,972
; FILING DATE: 26-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-6-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-079-511-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 5
US-08-467-607-1
; Sequence 1, Application US/08467607
; Patent No. 5783434
; GENERAL INFORMATION:
; APPLICANT: TUNG, JAY S.
; APPLICANT: SINHA, SUKANTO
; APPLICANT: McCONLOGUE, LISA
; APPLICANT: TATSUNO, GWEN

APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,607
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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Query Match           100.0%;  Score 222;  DB 1;  Length 43;
Best Local Similarity 100.0%;  Pred. No. 8e-27;
Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
        |||||||||||||||||||||||||||||||||||||||||||||
Db      1 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

```

RESULT 6

US-08-404-831-1

; Sequence 1, Application US/08404831

; Patent No. 5817626

GENERAL INFORMATION:

; APPLICANT: Mark A. Findeis, Howard Benjamin, Marc B. Garnick,

APPICANT: Malcolm L. Gefter, Arvind Hundal, Laura Kasman,

APPLICANT: Gary Musso, Ethan R. Signer, and James Wakefield

; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide

Aggrega

; NUMBER OF SEQUENCES: 3

;**CORRESPONDENCE ADDRESS:**

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,831
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hanley, Elizabeth A. (EAH)
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: PPI-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-404-831-1

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Query Match           100.0%;  Score 222;  DB 2;  Length 43;
Best Local Similarity 100.0%;  Pred. No. 8e-27;
Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy              1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
                  ||||||| ||||||| ||||||| ||||||| ||||||| ||||| ||||| |
Db              1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

```

RESULT 7
US-08-602-264A-3
; Sequence 3, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S
DISEASE A
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS
AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-602-264A-3

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Query Match           100.0%;  Score 222;  DB 2;  Length 43;
Best Local Similarity 100.0%;  Pred. No. 8e-27;
Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

```

RESULT 8
US-08-469-362-1
; Sequence 1, Application US/08469362
; Patent No. 5849711
; GENERAL INFORMATION:
; APPLICANT: TUNG, JAY S.
; APPLICANT: SINHA, SUKANTO
; APPLICANT: McCONLOGUE, LISA
; APPLICANT: SEMKO, CHRISTOPHER M.F.
; TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES

;
; STREET: 800 F. Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,362
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUVALL, JEAN M.
; REGISTRATION NUMBER: 32,731
; REFERENCE/DOCKET NUMBER: 002010-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-362-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 9
US-08-612-785B-1
; Sequence 1, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 10
US-08-475-579A-1
; Sequence 1, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
Aggrega
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-475-579A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 11
US-08-850-392-1
; Sequence 1, Application US/08850392.
; Patent No. 5858982
; GENERAL INFORMATION:
; APPLICANT: TUNG, JAY S.
; APPLICANT: SINHA, SUKANTO
; APPLICANT: McCONLOGUE, LISA
; APPLICANT: SEMKO, CHRISTOPHER M.F.
; TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES
; STREET: 800 F. Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,392
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,362
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DUVALL, JEAN M.
; REGISTRATION NUMBER: 32,731
; REFERENCE/DOCKET NUMBER: 002010-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-8370
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-850-392-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 12
US-08-986-948-6
; Sequence 6, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

;
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-6

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 13
US-08-975-977-1
; Sequence 1, Application US/08975977
; Patent No. 5965614
; GENERAL INFORMATION:
; APPLICANT: JAMES E. AUDIA
; APPLICANT: BEVERLY K. FOLMER
; APPLICANT: VARGHESE JOHN
; APPLICANT: LEE H. LATIMER

; APPLICANT: JEFFREY S. NISSEN
; APPLICANT: JON K. REEL
; APPLICANT: EUGENE D. THORSETT
; APPLICANT: CELIA A. WHITESITT
; TITLE OF INVENTION: N-(ARYL/HETEROARYL) AMINO
; TITLE OF INVENTION: ACID ESTERS, PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
; TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
; TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS
; TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker &
; ADDRESSEE: Mathis, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,977
; FILING DATE: Unassigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,444
; FILING DATE: 22 No. 5965614ember 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 002010-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-854-7400
; TELEFAX: 650-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-975-977-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 14

US-08-817-423-1

; Sequence 1, Application US/08817423

; Patent No. 5972634

; GENERAL INFORMATION:

; APPLICANT: TANZI, RUDOLPH E.

; APPLICANT: BUSH, ASHLEY I.

; APPLICANT: MOIR, ROBERT D.

; TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's

; TITLE OF INVENTION: Disease: Assessment of A Abnormalities

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,423

; FILING DATE: 4-AUG-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US94/11895

; FILING DATE: 19-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609.4110000/REF/JUK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-08-817-423-1

Query Match 100.0%; Score 222; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 8e-27;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

||||||||||||||||||||||||||||||||||||||||||

Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 15

US-08-920-162A-1

; Sequence 1, Application US/08920162A

; Patent No. 5985242
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
; TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162A
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-920-162A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

Search completed: November 19, 2004, 17:00:24
Job time : 51.3191 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:35:52 ; Search time 43.9149 Seconds
(without alignments)
94.212 Million cell updates/sec

Title: US-09-830-954A-3

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGGVVIAT 43

Scoring table: BLOSUM62

Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query Score	Match	Length	DB	ID	Description
1	222	100.0	57	2	A60045	Alzheimer's diseas
2	222	100.0	57	2	F60045	Alzheimer's diseas
3	222	100.0	57	2	D60045	Alzheimer's diseas
4	222	100.0	57	2	E60045	Alzheimer's diseas
5	222	100.0	57	2	G60045	Alzheimer's diseas
6	222	100.0	57	2	B60045	Alzheimer's diseas
7	222	100.0	82	2	PQ0438	Alzheimer's diseas
8	222	100.0	695	1	A49795	Alzheimer's diseas
9	222	100.0	770	1	QRHUA4	Alzheimer's diseas
10	217	97.7	42	2	PN0512	beta-amyloid prote
11	203	91.4	695	2	A27485	Alzheimer's diseas
12	203	91.4	695	2	S00550	Alzheimer's diseas
13	203	91.4	747	2	JH0773	Alzheimer's diseas

14	133	59.9	33	2	S23094	beta-amyloid prote
15	64	28.8	755	2	AI3228	tryptophan 2-monoo
16	62	27.9	755	1	DAAGWT	tryptophan 2-monoo
17	62	27.9	755	1	QQAG4T	tryptophan 2-monoo
18	57	25.7	327	2	S11435	genome polyprotein
19	57	25.7	503	2	S73843	general amino acid
20	56.5	25.5	378	2	S61992	SLG1 protein - yea
21	55.5	25.0	297	2	G69525	formylmethanofuran
22	55.5	25.0	621	2	AF3016	Na+/H ⁺ antiporter
23	55.5	25.0	642	2	B98268	probable sodium/hy
24	55.5	25.0	678	2	G71526	3-methyl-2-oxobuta
25	55	24.8	291	2	F95015	glycosyl transfera
26	55	24.8	317	2	H97888	glycosyl transfera
27	55	24.8	488	2	S27652	probable aldehyde
28	55	24.8	738	2	C95936	conserved hypothet
29	55	24.8	3063	2	JS0166	genome polyprotein
30	54.5	24.5	678	2	C81683	3-methyl-2-oxobuta
31	54.5	24.5	832	2	H84848	phospholipase D [i
32	54	24.3	77	2	C97027	feoA-like protein,
33	54	24.3	284	2	S04723	genome polyprotein
34	54	24.3	316	2	D97865	hypothetical prote
35	54	24.3	322	2	E71647	hypothetical prote
36	54	24.3	763	2	AI3443	Na+/H ⁺ antiporter
37	53.5	24.1	245	2	AH1098	a probable phospho
38	53.5	24.1	245	2	AG1461	probable phospho-b
39	53.5	24.1	708	2	T24727	hypothetical prote
40	53.5	24.1	971	2	D70128	conserved hypothet
41	53	23.9	256	2	G96774	hypothetical prote
42	53	23.9	390	2	C75103	na+/h ⁺ antiporter
43	53	23.9	422	2	D72302	hypothetical prote
44	53	23.9	601	2	T02581	nodulin-like prote
45	53	23.9	1555	2	JT0959	polyprotein - pota

ALIGNMENTS

RESULT 1

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: A60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: A60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56125

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 2

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 3

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 4

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C;Species: Ovis sp. (sheep)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: E60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: E60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56130

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 5

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: G60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56126

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
|||||||||||||||||||||||||||||||||||||||||||||

Db 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 6

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C;Species: Ursus maritimus (polar bear)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: UNIPROT:Q29149; EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
|||||||||||||||||||||||||||||||||||||

Db 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 7

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.

A;Reference number: PQ0438; MUID:93075180; PMID:1445331

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 222; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.8e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 59

RESULT 8

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A49795

R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.

A;Reference number: A49795; MUID:91273117; PMID:1905108

A;Accession: A49795

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-695 <POD>

A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing

Query Match 100.0%; Score 222; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 639

RESULT 9

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644

R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775

A;Accession: S02260

A;Molecule type: DNA

A;Residues: 1-288,'V',365-770 <LEM1>

A;Cross-references: EMBL:X13466

A;Note: alternative splice form APP(695)

R;Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A;Reference number: S05194

A;Accession: S05194

A;Molecule type: DNA

A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>

A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360

A;Note: alternative splice form APP(695)

R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.

A;Reference number: A32277; MUID:89165870; PMID:2538123

A;Accession: A32277

A;Molecule type: DNA

A;Residues: 1-75 <LAF>

A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN: AAC13654.1;

PID:g516074

R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.

A;Reference number: A33260; MUID:89392030; PMID:2675837

A;Accession: A33260

A;Molecule type: DNA

A;Residues: 656-737 <JOH>

A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865

R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.

A;Reference number: A35486; MUID:90321244; PMID:2196878

A;Accession: A35486

A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated
from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated
from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMPVIAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.;
van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral
hemorrhage, Dutch type.
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary
Alzheimer's disease.
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.;
Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.;
Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma,
V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.;
Schellenberg, G.D.
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds
for the APP gene region.
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA

A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.;
Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a
cell-surface receptor.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and the neuritic plaque amyloid peptides.
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain
amyloid of Alzheimer's disease.
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop,
P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage
near the Alzheimer locus.
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang,
J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid
A4 precursor of Alzheimer's disease.

A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>

R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB: M18734; NID: g178572; PIDN: AAA51726.1; PID: g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 714

RESULT 10
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment for NK-1 substance p receptors.
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
A;Cross-references: UNIPROT:Q7M088
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid

Query Match 97.7%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIA 42

RESULT 11

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004

C;Accession: A27485; S19727; I49485

R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A;Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: UNIPROT:P12023; GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085

A;Experimental source: brain

R;de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A;Reference number: S19727; MUID:92096458; PMID:1756177

A;Accession: S19727

A;Molecule type: mRNA

A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695

<STR>

A;Cross-references: EMBL:X59379

R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.

Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A;Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329

C;Genetics:

A;Map position: 16C3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 91.4%; Score 203; DB 2; Length 695;
Best Local Similarity 93.0%; Pred. No. 1.5e-18;
Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
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Db 597 DAEFGHDGSGFEVRHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 639

RESULT 12

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.;
Seuberg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in
rat brain suggests a role in cell contact.
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: UNIPROT:P08592; EMBL:X07648; NID:g55616; PIDN:CAA30488.1;
PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate
proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempaska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of
rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 91.4%; Score 203; DB 2; Length 695;
Best Local Similarity 93.0%; Pred. No. 1.5e-18;
Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||||:|| ||||||||||||| |||||||||
Db 597 DAEFGHDGFEVRHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 639

RESULT 13
JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 91.4%; Score 203; DB 2; Length 747;
Best Local Similarity 88.4%; Pred. No. 1.7e-18;
Matches 38; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
|:|:|||:|||||||||:|||||||||:|||||||||
Db 649 DSEYRHDTAYEVHHQKLVFFAEEVGSNKGAIIGLMVGGVVIAT 691

RESULT 14
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase.
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 59.9%; Score 133; DB 2; Length 33;
Best Local Similarity 89.3%; Pred. No. 7.9e-11;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28
||||| ||||:||| |||||||||||
Db 6 DAEFGHDSGFEVRHQKLVFFAEDVGSNK 33

RESULT 15
AI3228

tryptophan 2-monooxygenase tms1 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid Ti
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Accession: AI3228
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelland, E.; Palmieri, A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey, S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-755 <KUR>
A;Cross-references: UNIPROT:Q8U6A3; GB:AE008690; PIDN:AAL46247.1; PID:g17744025; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: tms1
A;Genome: plasmid
C;Superfamily: Tryptophan 2-monooxygenase

Query Match 28.8%; Score 64; DB 2; Length 755;
Best Local Similarity 43.2%; Pred. No. 2.7;
Matches 16; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

Qy 7 DSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
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Db 223 DSG-----RIGFFPEDVPKPKVAIIGAGISGLVVAS 253

Search completed: November 19, 2004, 16:59:19
Job time : 44.9149 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:58:33 ; Search time 179.319 Seconds
(without alignments)
84.918 Million cell updates/sec

Title: US-09-830-954A-3

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGGVVIAT 43

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	222	100.0	43	9	US-09-280-966-1	Sequence 1, Appli
2	222	100.0	43	9	US-09-904-987-1	Sequence 1, Appli
3	222	100.0	43	9	US-09-808-037-3	Sequence 3, Appli
4	222	100.0	43	9	US-09-866-712-3	Sequence 3, Appli
5	222	100.0	43	9	US-09-972-475-1	Sequence 1, Appli
6	222	100.0	43	9	US-09-992-800-1	Sequence 1, Appli
7	222	100.0	43	9	US-09-895-443-1	Sequence 1, Appli
8	222	100.0	43	9	US-09-915-342-1	Sequence 1, Appli
9	222	100.0	43	9	US-09-996-357-1	Sequence 1, Appli
10	222	100.0	43	9	US-09-992-994-1	Sequence 1, Appli
11	222	100.0	43	9	US-09-984-834-1	Sequence 1, Appli
12	222	100.0	43	10	US-09-425-956-1	Sequence 1, Appli
13	222	100.0	43	10	US-09-942-253-1	Sequence 1, Appli
14	222	100.0	43	13	US-10-041-605-1	Sequence 1, Appli
15	222	100.0	43	13	US-10-076-708-7	Sequence 7, Appli
16	222	100.0	43	13	US-10-051-496-1	Sequence 1, Appli
17	222	100.0	43	14	US-10-217-459-1	Sequence 1, Appli
18	222	100.0	43	14	US-10-162-889-3	Sequence 3, Appli
19	222	100.0	43	14	US-10-217-584-1	Sequence 1, Appli
20	222	100.0	43	14	US-10-326-049-1	Sequence 1, Appli
21	222	100.0	43	14	US-10-190-548A-2	Sequence 2, Appli
22	222	100.0	43	14	US-10-335-035-1	Sequence 1, Appli
23	222	100.0	43	14	US-10-267-017-1	Sequence 1, Appli
24	222	100.0	43	14	US-10-314-221-1	Sequence 1, Appli
25	222	100.0	43	14	US-10-437-706-2	Sequence 2, Appli
26	222	100.0	43	14	US-10-385-065-1	Sequence 1, Appli
27	222	100.0	43	15	US-10-463-729-1	Sequence 1, Appli
28	222	100.0	43	15	US-10-355-700-1	Sequence 1, Appli
29	222	100.0	43	15	US-10-384-788-3	Sequence 3, Appli
30	222	100.0	43	15	US-10-618-856-3	Sequence 3, Appli
31	222	100.0	43	15	US-10-415-383-2	Sequence 2, Appli
32	222	100.0	43	15	US-10-619-454-2	Sequence 2, Appli
33	222	100.0	43	16	US-10-250-581-1	Sequence 1, Appli
34	222	100.0	43	16	US-10-699-517-33	Sequence 33, Appli
35	222	100.0	43	16	US-10-796-522-1	Sequence 1, Appli
36	222	100.0	53	9	US-09-797-543-5	Sequence 5, Appli
37	222	100.0	53	13	US-10-016-717-1	Sequence 1, Appli
38	222	100.0	56	17	US-10-771-174A-16	Sequence 16, Appli
39	222	100.0	56	17	US-10-771-174A-19	Sequence 19, Appli
40	222	100.0	58	17	US-10-771-174A-12	Sequence 12, Appli
41	222	100.0	58	17	US-10-771-174A-14	Sequence 14, Appli
42	222	100.0	58	17	US-10-771-174A-27	Sequence 27, Appli
43	222	100.0	59	9	US-09-975-932-1	Sequence 1, Appli
44	222	100.0	60	17	US-10-771-174A-20	Sequence 20, Appli
45	222	100.0	64	17	US-10-771-174A-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
 US-09-280-966-1
 ; Sequence 1, Application US/09280966
 ; Patent No. US20010020097A1

; GENERAL INFORMATION:

; APPLICANT: JAMES E. AUDIA
; BEVERLY K. FOLMER
; VARGHESE JOHN
; JEFFREY S. NISSEN
; WARREN J. PORTER
; EUGENE D. THORSETT
; JING WU

; TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL) AMINO
; ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
; COMPRISING SAME, AND METHODS FOR INHIBITING
; -AMYLOID PEPTIDE RELEASE AND/OR ITS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/280,966
; FILING DATE: 30-Mar-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/976,191
; FILING DATE: 21 NOV 1997
; APPLICATION NUMBER: 60/077,175
; FILING DATE: 22 NOV 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 002010-335

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-622-2300
; TELEFAX: 650-622-2499

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-280-966-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 2

US-09-904-987-1

; Sequence 1, Application US/09904987
; Patent No. US20020037908A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020037908A1actyl, Inc.
; TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathological
; TITLE OF INVENTION: Protein Assembly or Aggregation
; FILE REFERENCE: 42108/26146
; CURRENT APPLICATION NUMBER: US/09/904,987
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4
; DATABASE ENTRY DATE: 2000-09-15
; RELEVANT RESIDUES: (672)..(714)

US-09-904-987-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 3

US-09-808-037-3

; Sequence 3, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR
DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3

; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQQLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQQLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 4

US-09-866-712-3

; Sequence 3, Application US/09866712
; Patent No. US20020058637A1
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY
; INHIBITING NEURONAL CELL DEATH AND TREATING
ALZHEIMER'S DISEASE AND TAU-PROTEIN
; KINASE I (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/866,712
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/216,958
; FILING DATE: December 21, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-866-712-3

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 5

US-09-972-475-1

; Sequence 1, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1784
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,443
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/356,931
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/897,342
FILING DATE: 21-JUL-1997
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Jr., Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-016CP4CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Query Match           100.0%;  Score 222;  DB 9;  Length 43;
Best Local Similarity 100.0%;  Pred. No. 7.6e-23;
Matches   43;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

Qy      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| .
Db      1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

```

RESULT 8
US-09-915-342-1
; Sequence 1, Application US/09915342
; Publication No. US20020123486A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Jinq

; APPLICANT: Tung, Jay S.
; APPLICANT: Thorsett, Eugene D.
; APPLICANT: Nissen, Jeffrey S.
; APPLICANT: Neitz, Jeffrey
; APPLICANT: Latimer, Lee H.
; APPLICANT: John, Varghese
; APPLICANT: Britton, Thomas C.
; APPLICANT: Audia, James A.
; APPLICANT: Reel, Jon K.
; APPLICANT: Mabry, Thomas E.
; APPLICANT: Cwi, Cynthia L.
; APPLICANT: McDaniel, Stacey L.
; APPLICANT: Scott, William Leonard
; TITLE OF INVENTION: Cycloalkyl, Lactam, Lactone and Related Compounds,
; TITLE OF INVENTION: Pharmaceutical Compositions Comprising Same, and
; TITLE OF INVENTION: Methods of Inhibiting Beta-Amyloid Peptide Release
; TITLE OF INVENTION: and/or its Synthesis by Use of Such Compounds
; FILE REFERENCE: 002010-062
; CURRENT APPLICATION NUMBER: US/09/915,342
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US/08/996,422
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/064,851
; PRIOR FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: beta-amyloid precursor protein (APP)
US-09-915-342-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 9
US-09-996-357-1
; Sequence 1, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gefter, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 10

US-09-992-994-1

; Sequence 1, Application US/09992994
; Patent No. US20020136718A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2005
; CURRENT APPLICATION NUMBER: US/09/992,994
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-994-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 11

US-09-984-834-1

; Sequence 1, Application US/09984834

; Patent No. US20020137743A1
; GENERAL INFORMATION:
; APPLICANT: JING WU
; EUGENE D. THORSETT
; JEFFREY S. NISSEN
; THOMAS E. MABRY
; LEE H. LATIMER
; VARGHESE JOHN
; LAWRENCE Y. FANG
; JAMES E. AUDIA
; TITLE OF INVENTION: N-(ARYL/HETEROARYLACETYL)
; AMINO ACID ESTERS, PHARMACEUTICAL
; COMPOSITIONS COMPRISING SAME, AND
; METHODS FOR INHIBITING BETA-AMYLOID
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker &
; Mathis, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,834
; FILING DATE: 31-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,179
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 002010-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-622-2300
; TELEFAX: 650-622-2499
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-984-834-1

Query Match 100.0%; Score 222; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

Db

||||||||||||||||||||||||||||||||||||||||||
1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 12

US-09-425-956-1

; Sequence 1, Application US/09425956

; Publication No. US20030073074A1

; GENERAL INFORMATION:

; APPLICANT: TANZI, RUDOLPH E.

; APPLICANT: BUSH, ASHLEY I.

; APPLICANT: MOIR, ROBERT D.

; TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's

; TITLE OF INVENTION: Disease: Assessment of A Abnormalities

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/425,956

; FILING DATE: Herewith (25-OCT-1999)

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/817,423

; FILING DATE: 04-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US94/11895

; FILING DATE: 19-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0609.4110001/REF/JUK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-09-425-956-1

Query Match 100.0%; Score 222; DB 10; Length 43;

Best Local Similarity 100.0%; Pred. No. 7.6e-23;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
|||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 13

US-09-942-253-1

; Sequence 1, Application US/09942253
; Publication No. US20030082191A1
; GENERAL INFORMATION:
; APPLICANT: Poduslo, Joseph F.
; APPLICANT: Curran, Geoffry L.
; TITLE OF INVENTION: TREATMENT FOR CENTRAL NERVOUS SYSTEM DISORDERS
; FILE REFERENCE: 07039-351001
; CURRENT APPLICATION NUMBER: US/09/942,253
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-942-253-1

Query Match 100.0%; Score 222; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
|||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 14

US-10-041-605-1

; Sequence 1, Application US/10041605
; Publication No. US20020115223A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bush, Ashley I.
; TITLE OF INVENTION: An In Vitro System For Determining Formation of A
Amyloid
; FILE REFERENCE: 0609.4100001
; CURRENT APPLICATION NUMBER: US/10/041,605
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 08/294,819
; PRIOR FILING DATE: 1994-08-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-041-605-1

Query Match 100.0%; Score 222; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

RESULT 15

US-10-076-708-7

; Sequence 7, Application US/10076708
; Publication No. US20020164657A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Satish
; APPLICANT: Rank, Kenneth
; TITLE OF INVENTION: Assays for Accessing Aa-Tau Aggregation
; FILE REFERENCE: 6322
; CURRENT APPLICATION NUMBER: US/10/076,708
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-076-708-7

Query Match 100.0%; Score 222; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 7.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43

Search completed: November 19, 2004, 17:15:19

Job time : 180.319 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 16:35:27 ; Search time 230.553 Seconds
(without alignments)
107.312 Million cell updates/sec

Title: US-09-830-954A-3

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGGVVIAT 43

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	222	100.0	57	1	A4_URSMA	Q29149 ursus marit
2	222	100.0	58	1	A4_CANFA	Q28280 canis famil
3	222	100.0	58	1	A4_RABIT	Q28748 oryctolagus
4	222	100.0	58	1	A4_SHEEP	Q28757 ovis aries
5	222	100.0	59	1	A4_BOVIN	Q28053 bos taurus
6	222	100.0	113	2	Q8JH58	Q8jh58 chelydra se
7	222	100.0	534	2	O93296	O93296 gallus gall
8	222	100.0	695	2	Q6RH29	Q6rh29 canis famil
9	222	100.0	695	2	Q9DGJ8	Q9dgj8 gallus gall
10	222	100.0	695	2	AAR97727	Aar97727 canis fam
11	222	100.0	751	1	A4_SAISC	Q95241 s amyloid b
12	222	100.0	751	2	Q6RH28	Q6rh28 canis famil
13	222	100.0	751	2	Q9DGJ7	Q9dgj7 gallus gall
14	222	100.0	751	2	AAR97728	Aar97728 canis fam
15	222	100.0	751	2	AAH65529	Aah65529 homo sapi

16	222	100.0	770	1	A4_CAVPO	Q60495 c amyloid b
17	222	100.0	770	1	A4_HUMAN	P05067 h amyloid b
18	222	100.0	770	1	A4_MACFA	P53601 m amyloid b
19	222	100.0	770	1	A4_PIG	P79307 s amyloid b
20	222	100.0	770	2	Q6RH30	Q6rh30 canis famil
21	222	100.0	770	2	AAR97726	Aar97726 canis fam
22	217	97.7	42	2	Q7M088	Q7m088 cavia porce
23	217	97.7	569	2	Q9PVL1	Q9pvl1 gallus gall
24	203	91.4	79	2	O35463	O35463 cricetus
25	203	91.4	218	2	Q8BPV5	Q8bpv5 mus musculu
26	203	91.4	384	2	Q8BPC7	Q8bpc7 mus musculu
27	203	91.4	693	2	Q98SG0	Q98sg0 xenopus lae
28	203	91.4	695	2	AAH70409	Aah70409 mus muscu
29	203	91.4	733	2	Q6P6Q5	Q6p6q5 rattus norv
30	203	91.4	733	2	AAH62082	Aah62082 rattus no
31	203	91.4	747	2	Q91963	Q91963 xenopus. ap
32	203	91.4	749	2	Q6NRR1	Q6nrr1 xenopus lae
33	203	91.4	749	2	AAH70668	Aah70668 xenopus l
34	203	91.4	750	2	Q6DJB6	Q6djb6 xenopus tro
35	203	91.4	770	1	A4_MOUSE	P12023 m amyloid b
36	203	91.4	770	1	A4_RAT	P08592 r amyloid b
37	203	91.4	770	2	AAM90259	Aam90259 rattus no
38	203	91.4	770	2	AAP23169	Aap23169 mus muscu
39	200	90.1	695	2	Q7ZXQ0	Q7zxq0 xenopus lae
40	200	90.1	695	2	Q98SF9	Q98sf9 xenopus lae
41	193	86.9	699	2	O57394	O57394 narke japon
42	180	81.1	780	1	A4_TETFL	073683 tetraodon f
43	176	79.3	33	2	Q9UC33	Q9uc33 homo sapien
44	176	79.3	737	1	A4_FUGRU	093279 fugu rubrip
45	162.5	73.2	357	2	Q8UUI8	Q8uui8 brachydanio

ALIGNMENTS

RESULT 1

A4_URSMA

ID A4_URSMA STANDARD; PRT; 57 AA.

AC Q29149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

DE Name=APP;

OS Ursus maritimus (Polar bear) (Thalarctos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC --!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC --!- SUBCELLULAR LOCATION: Type I membrane protein.
CC --!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56128; CAA39593.1; -.
DR PIR; B60045; B60045.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 Beta-amyloid protein (Potential).
FT DOMAIN <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.5e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 2

A4_CANFA

ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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DR EMBL; X56125; CAA39590.1; -.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Amyloid; Glycoprotein; Transmembrane.

FT NON_TER 1 1
FT CHAIN 7 49 Beta-amyloid protein (Potential).
FT DOMAIN <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 49

RESULT 3

A4_RABIT

ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC --!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC --!- SIMILARITY: Belongs to the APP family.
 CC -----
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 CC -----
 DR EMBL; X56129; CAA39594.1; -.
 DR HSSP; P08592; 1NMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Glycoprotein; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 Beta-amyloid protein (Potential).
 FT DOMAIN <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT DOMAIN 58 >58 Cytoplasmic (Potential).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

 Query Match 100.0%; Score 222; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.6e-21;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
 |||||||
 Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

 RESULT 4
 A4_SHEEP
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 Beta-amyloid protein (Potential).
FT DOMAIN <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT DOMAIN 58 >58 Cytoplasmic (Potential).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 48

RESULT 5

A4_BOVIN

ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TAXID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
intracellular signaling pathway through the GTP-binding protein
G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
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CC -----
DR EMBL; X56124; CAA39589.1; -.
DR EMBL; X56126; CAA39591.1; -.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 Beta-amyloid protein (Potential).
FT DOMAIN <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT DOMAIN 59 >59 Cytoplasmic (Potential).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 222; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 49

RESULT 6

Q8JH58

ID Q8JH58 PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
protein family in the hypothalamus of the snapping turtle, Chelydra
serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275 (2002).
DR EMBL; AF541917; AAN04908.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 DAEFRHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 57

RESULT 7

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTR; 1.
FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 478

RESULT 8

Q6RH29

ID Q6RH29 PRELIMINARY; PRT; 695 AA.
AC Q6RH29;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP695.
GN Name=beta APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakata M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY498707; AAR97727.1; -.

DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;

 Query Match 100.0%; Score 222; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
 |||||||
 Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 639

RESULT 9
 Q9DGJ8
 ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-amyloid protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AF289218; AAG00593.1; -.
 DR HSSP; P08592; 1NMJ.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

 Query Match 100.0%; Score 222; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 639

RESULT 10

AAR97727

ID AAR97727 PRELIMINARY; PRT; 695 AA.
AC AAR97727;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP695.
GN BETA APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakata M.;
RT "Sequence analysis and chromosomal mapping of presenilin-1 and amyloid
precursor protein genes in dogs.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY498707; AAR97727.1; -.
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 639

RESULT 11

A4_SAISC

ID A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
secretase C-terminal fragment 50); C31].
GN Name=APP;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral
RT amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metallated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, and SHC1, Numb and Dabl (By similarity). Binding
CC to Dabl inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=Q95241-1; Sequence=Displayed;

CC Name=APP695;
CC IsoId=Q95241-2; Sequence=Not described;
CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -!- SIMILARITY: Belongs to the APP family.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S81024; AAD14347.1; -.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Alternative splicing; Amyloid; Apoptosis; Cell adhesion; Coated pits;
 KW Copper; Endocytosis; Glycoprotein; Heparin-binding; Iron;
 KW Metal-binding; Phosphorylation; Proteoglycan;
 KW Serine protease inhibitor; Signal; Transmembrane; Zinc.
 FT SIGNAL 1 17 By similarity.
 FT CHAIN 18 751 Amyloid beta A4 protein.
 FT CHAIN 18 668 Soluble APP-alpha (Potential).
 FT CHAIN 18 652 Soluble APP-beta (Potential).
 FT CHAIN 653 751 C99 (Potential).
 FT CHAIN 653 694 Beta-amyloid protein 42 (Potential).
 FT CHAIN 653 692 Beta-amyloid protein 40 (Potential).
 FT CHAIN 669 751 C83 (Potential).
 FT CHAIN 669 694 P3(42) (Potential).
 FT CHAIN 669 692 P3(40) (Potential).
 FT CHAIN 693 751 Gamma-CTF(59) (Potential).
 FT CHAIN 695 751 Gamma-CTF(57) (Potential).
 FT CHAIN 702 751 Gamma-CTF(50) (Potential).
 FT CHAIN 721 751 C31 (Potential).
 FT DOMAIN 18 680 Extracellular (Potential).
 FT TRANSMEM 681 704 Potential.
 FT DOMAIN 705 751 Cytoplasmic (Potential).
 FT DOMAIN 96 110 Heparin-binding (By similarity).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/Kunitz inhibitor.
 FT DOMAIN 316 344 Heparin-binding (By similarity).
 FT DOMAIN 363 428 Heparin-binding (By similarity).
 FT DOMAIN 504 521 Collagen-binding (By similarity).
 FT DOMAIN 713 732 Interaction with G(o)-alpha (By similarity).
 FT DOMAIN 230 260 Asp/Glu-rich (acidic).
 FT DOMAIN 274 280 Poly-Thr.
 FT SITE 144 144 Required for copper(II) reduction (By similarity).
 FT SITE 301 302 Reactive bond.
 FT SITE 652 653 Cleavage (by beta-secretase) (By similarity).
 FT SITE 653 654 Cleavage (by caspase-6) (By similarity).
 FT SITE 668 669 Cleavage (by alpha-secretase) (By similarity).
 FT SITE 685 685 Involved in free radical propagation (By similarity).
 FT SITE 687 687 Involved in oxidative reactions (By similarity).

FT SITE	692	693	Cleavage (by gamma-secretase; site 1) (By similarity).
FT SITE	694	695	Cleavage (by gamma-secretase; site 2) (By similarity).
FT SITE	701	702	Cleavage (by gamma-secretase; site 3) (By similarity).
FT SITE	705	715	Basolateral sorting signal (By similarity).
FT SITE	720	721	Cleavage (by caspases-3, -6, -8 or -9) (By similarity).
FT SITE	738	741	Endocytosis signal.

Query Match 100.0%; Score 222; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 3.3e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
 |||||||||||||||||||||||||||||||||||||||||||
 Db 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 695

RESULT 12

Q6RH28

ID Q6RH28 PRELIMINARY; PRT; 751 AA.
 AC Q6RH28;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Beta amyloid protein isoform APP751.
 GN Name=beta APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakata M.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AY498708; AAR97728.1; -.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 751 AA; 84832 MW; 7541A947B46DA5A4 CRC64;
Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 43
|||||||||||||||||||||||||||||||||||||||||
Db 653 DAEFRHDSGYEVHQKLVFFAEDVGSNKGAIIGLMVGGVVIAT 695

RESULT 13

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
AC Q9DGJ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC --!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF289219; AAG00594.1; -.
DR HSSP; P08592; 1NMJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTR; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 695

RESULT 14

AAR97728

ID AAR97728 PRELIMINARY; PRT; 751 AA.
AC AAR97728;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta amyloid protein isoform APP751.
GN BETA APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakata M.;
RT "Sequence analysis and chromosomal mapping of presenilin-1 and amyloid
precursor protein genes in dogs.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY498708; AAR97728.1; -.
SQ SEQUENCE 751 AA; 84832 MW; 7541A947B46DA5A4 CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 695

RESULT 15

AAH65529

ID AAH65529 PRELIMINARY; PRT; 751 AA.
AC AAH65529;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid beta A4 protein, isoform b.
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC065529; AAH65529.1; -.
SQ SEQUENCE 751 AA; 84818 MW; C987C557C5A3714E CRC64;

Query Match 100.0%; Score 222; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 43
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIAT 695

Search completed: November 19, 2004, 16:58:25
Job time : 230.553 secs